

(FILE 'HOME' ENTERED AT 14:18:51 ON 29 NOV 2004)

FILE 'MEDLINE, CAPLUS, BIOSIS, AGRICOLA' ENTERED AT 14:18:55 ON 29 NOV  
2004

L1 88921 S ZEA (2N) MAYS  
L2 25 S L1 AND EXONUCLEASE  
L3 17 DUP REM L2 (8 DUPLICATES REMOVED)

Database : UniProt\_02:\*  
 1: uniprot\_sprot:\*  
 2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2284	79.7	705	2	Q7XQR9	Q7xqr9 oryza sativ
2	2020.5	70.5	720	1	MR11_ARATH	Q9xgm2 arabidopsis
3	1571.5	54.9	615	2	Q6ZBS2	Q6zbs2 oryza sativ
4	1571.5	54.9	615	2	BAD03045	Bad03045 oryza sat
5	1571.5	54.9	615	2	BAD03241	Bad03241 oryza sat
6	958.5	33.5	708	1	MR11_HUMAN	P49959 homo sapien
7	958.5	33.5	708	2	AAH63458	Aah63458 homo sapi
8	958.5	33.5	708	2	AAS79320	Aas79320 homo sapi
9	949	33.1	706	1	MR11_MOUSE	Q61216 mus musculu
10	948.5	33.1	711	1	MR11_XENLA	Q9w6k1 xenopus lae
11	946	33.0	513	2	Q8BRV3	Q8brv3 mus musculu
12	940	32.8	706	1	MR11_RAT	Q9jim0 rattus norv
13	929.5	32.5	619	2	Q7T397	Q7t397 brachydanio
14	919.5	32.1	731	1	MR11_COPCI	Q9uvm9 coprinus ci
15	907.5	31.7	700	1	MR11_CHICK	Q9iam7 gallus gall

Database :       PIR\_79:\*  
               1:  pir1:\*  
               2:  pir2:\*  
               3:  pir3:\*  
               4:  pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	2020.5	70.5		720	2	T52564	Mre11 protein homo
2	852.5	29.8		649	1	S58097	probable dna repai
3	768	26.8		692	1	S57592	probable phosphoes
4	724	25.3		772	2	T27512	hypothetical prote
5	178	6.2		443	1	G69378	probable phosphoes
6	175.5	6.1		423	2	E75103	phosphoesterase ho
7	174.5	6.1		413	1	D71083	probable phosphoes
8	163.5	5.7		587	1	E69171	phosphoesterase-re
9	150.5	5.3		381	2	C90395	DNA repair protein
10	143	5.0		1038	2	JC5497	claustrin - chicke

RESULT 4

US-10-425-115-230925

; Sequence 230925, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 230925

; LENGTH: 726

; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(726)

; OTHER INFORMATION: unsure at all Xaa locations

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577\_142196C.1.pep

US-10-425-115-230925

Query Match 88.7%; Score 2539; DB 17; Length 726;

Best Local Similarity 90.6%; Pred. No. 1.3e-199;

Matches 499; Conservative 0; Mismatches 0; Indels 52; Gaps 2;

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Qy      25 MSEPAPSGGEGDVNTRLILVATDCHLGYMEKDEIRRFDSFQAFEEICALADKNKVDFIL 84
      |||
Db      1 MSEPAPSGGEGDVNTRLILVATDCHLGYMEKDEIRRFDSFQAFEEICALADKNKVDFIL 60

Qy      85 LGGDLFHENKPSRSTLVKTIEILRRYCLNDQPVKFQVVSQDQTVNFPNRFQVNYEDPNFN 144
      |||
Db      61 LGGDLFHENKPSRSTLVKTIEILRRYCLNDQPVKFQVVSQDQTVNFPNRFQVNYEDPNFN 120

Qy     145 VGLPVFTIHGNHDDPAGVDNLSAIDILSACNLVNYFGKMDLGGSGVGQIAVYPVLVKKGM 204
      |||
Db     121 VGLPVFTIHGNHDDPAGVDNLSAIDILSACNLVNYFGKMDLGGSGVGQIAVYPVLVKKGM 180

Qy     205 TSVALYGLGNIRDERLNRMFQTPHSVQWMPGTQDGESASDWFNVLVHQNRIKTNPKSA 264
      |||
Db     181 TSVALYGLGNIRDERLNRMFQTPHSVQWMPGTQDGESASDWFNVLVHQNRIKTNPKSA 240

Qy     265 INEHFL-----PGSSVATSLIDGEAKPKHVLLLE 293
      |||
Db     241 INEHFLPRFLDFIVWGHEHECLIDPQEVPGMGFHITQPGSSVATSLIDGEAKPKHVLLLE 300

Qy     294 IKGNQYRPTKIPLRSVRPFYAEVVLKDEADVNSNDQDSVLEHLDKIVRNLIKSSQPTA 353
      |||
Db     301 IKGNQYRPTKIPLRSVRPFYAEVVLKDEADVNSNDQDSVLEHLDKIVRNLIKSSQPTA 360

Qy     354 SRSEPKLPLVRIKVDYSGFSTINPQRFQKYVGKVANPQDILIFSKSAKKRQTTGDHIDD 413

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Db 361 |||||SRSEPKLPLVRIKVDYSGFSTINPQRFQKYVGKVANPQDILIFSKSAKKRQTTGDHIDD 420

Qy 414 SEKLRPEELNQQTIEALVAESNL-----KMEILPVDDL DIALHD 452

Db 421 |||||SEKLRPEELNQQTIEALVAESNLXFTAHYLDMRMMFCEDHFIFXKMEILPVDDL DIALHD 480

Qy 453 FVNKDDKMAFYSLQRNLEETRNLKSSEADKSKFEEEDIIVKVGECMQERVKERSLHSD 512

Db 481 |||||FVNKDDKMAFYSLQRNLEETRNLKSSEADKSKFEEEDIIVKVGECMQERVKERSLHSD 540

Qy 513 GTRLTTGSHNL 523

Db 541 |||||GTRLTTGSHNL 551

Database :           Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	2864	100.0		552	9	US-09-835-654-2	Sequence 2, Appli
2	2864	100.0		552	15	US-10-650-108-2	Sequence 2, Appli
3	2864	100.0		552	16	US-10-650-109-2	Sequence 2, Appli
4	2539	88.7		726	17	US-10-425-115-230925	Sequence 230925,
5	2201.5	76.9		490	15	US-10-425-114-53913	Sequence 53913, A
6	2200.5	76.8		497	15	US-10-425-114-64871	Sequence 64871, A
7	2135.5	74.6		554	16	US-10-437-963-184295	Sequence 184295,
8	2020.5	70.5		720	13	US-10-047-412A-8	Sequence 8, Appli
9	1571.5	54.9		615	16	US-10-437-963-204901	Sequence 204901,
10	958.5	33.5		708	13	US-10-087-192-1224	Sequence 1224, Ap
11	950	33.2		752	13	US-10-087-192-1221	Sequence 1221, Ap

Database :        Issued\_Patents\_AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	2864	100.0	552	4	US-09-835-654-2	Sequence 2, Appli
2	2020.5	70.5	720	3	US-09-480-921B-8	Sequence 8, Appli
3	954.5	33.3	680	4	US-09-538-092-1165	Sequence 1165, Ap
4	768	26.8	692	4	US-09-538-092-632	Sequence 632, App
5	507.5	17.7	270	4	US-09-248-796A-19151	Sequence 19151, A
6	141.5	4.9	132	4	US-09-270-767-33195	Sequence 33195, A
7	141.5	4.9	132	4	US-09-270-767-48412	Sequence 48412, A
8	136	4.7	857	4	US-09-248-796A-20522	Sequence 20522, A
9	122	4.3	1120	3	US-09-147-404-1	Sequence 1, Appli
10	122	4.3	1935	4	US-09-538-092-916	Sequence 916, App
11	121	4.2	398	4	US-09-710-279-44	Sequence 44, Appl
12	121	4.2	398	4	US-09-710-279-1498	Sequence 1498, Ap
13	121	4.2	417	3	US-09-134-001C-3810	Sequence 3810, Ap

US-09-480-921B-8

US-09-480-921B-8

Matches 385; Conservative 62; Mismatches 37; Indels 35; Gaps 4;

427 EALVAESNLKMEILPVDLDVALHNFVNKDDKLAFYSCVQYNLQETRGLAKDSDAKKFE 486



Qy            488 EEDIIVKVGECMQERVKERSLHSKDGTR-LTTG--SHNL 523  
             |:|:|:|||||:::||:|:|:|                 :: |:| | ||  
Db            487 EDDLILKVGECLERLKDRSTRPTGSSQFLSTGLTSEN 525

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result			%				ID	Description
	No.	Score	Query	Match	Length	DB		
1		3616	100.0	3616	6	AX460870	AX460870	Sequence
2		3529.8	97.6	3665	9	BC013153	BC013153	Homo sapi
3		3505.4	96.9	3607	6	BD175095	BD175095	Nucleic a
4		2844.4	78.7	2976	6	AX323479	AX323479	Sequence
5		2665.6	73.7	2736	9	AY036093	AY036093	Homo sapi
6		2597.2	71.8	2603	6	AX377787	AX377787	Sequence
7		2567.6	71.0	2592	6	AX817285	AX817285	Sequence
8		2461.4	68.1	2599	6	AX817283	AX817283	Sequence
9		2443.6	67.6	3608	4	AF529202	AF529202	Bos tauru
10		2309	63.9	2402	6	AX780632	AX780632	Sequence
11		2269.4	62.8	2271	9	AF338441	AF338441	Homo sapi
12		2265.4	62.6	2322	9	BC007522	BC007522	Homo sapi
13		2263.2	62.6	2268	6	AX323481	AX323481	Sequence
14		2258.2	62.5	2271	9	AF395336	AF395336	Homo sapi
15		2019.6	55.9	2059	9	AK025542	AK025542	Homo sapi
16		1918.8	53.1	3767	6	BD269865	BD269865	The poly
17		1730	47.8	2274	6	BD175096	BD175096	Nucleic a
18		1730	47.8	2274	10	AF338440	AF338440	Mus muscu